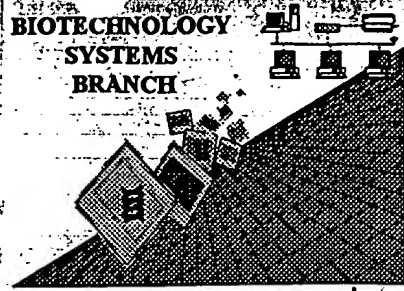


BEST AVAILABLE COPY

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



STIC MAIL ROOM

Aug - 8 2000

RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/509,449

Source:

1643

Date Processed by STIC:

7/24/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/509449

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES) 3, 4, 5, 6, 9
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1643

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/509,449

DATE: 07/24/2000
TIME: 13:38:40

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07242000\I509449.raw

*Suggestion: Consult
new sequence
Does Not Comply
Corrected Diskette Needed*

3 <110> APPLICANT: Tonen Corporation
5 <120> TITLE OF INVENTION: Method for Measurement of hepatitis C virus
7 <130> FILE REFERENCE: G902
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/509,449
C--> 9 <141> CURRENT FILING DATE: 2000-03-28
9 <150> PRIOR APPLICATION NUMBER: JP-10-216094
10 <151> PRIOR FILING DATE: 1998-07-30
E--> 12 <160> NUMBER OF SEQ ID NOS: 9

*See item 5
on Enva
summary
sheet*

ERRORED SEQUENCES

111 <210> SEQ ID NO: 6
112 <211> LENGTH: 20
113 <212> TYPE: PRT
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
E--> 118 <230> *22307 is an invalid numerical identifier.*
W--> 120 <400> SEQUENCE: 6
E--> 121 Asp Pro Arg His Arg Ser Arg Asn Val Gly Lys Val Lle Asp Thr Leu
122 1 5 10 15
123 Thr Cys Gly Phe
124 20
126 <210> SEQ ID NO: 7
127 <211> LENGTH: 24
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
W--> 131 <220> FEATURE: Probe
E--> 133 <230> Synthetic DNA
W--> 135 <223> OTHER INFORMATION:
135 <400> SEQUENCE: 7
136 gaattcatgg gcacgaatcc taaa
138 <210> SEQ ID NO: 8
139 <211> LENGTH: 21
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
W--> 143 <220> FEATURE: Probe
E--> 145 <230> Synthetic DNA
W--> 147 <223> OTHER INFORMATION:
147 <400> SEQUENCE: 8
148 ttagtctctcc agaaccgga c
150 <210> SEQ ID NO: 9
151 <211> LENGTH: 16
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:

*see item 12 on Enva
summary*

*Use <2237
when explaining
source material
of Artificial
Sequence*

*<2207 does not have a
response. It is a "leader" only.*

*Insert all
explanations of
source material
on same line as <2237.*

same Enva

see item 12 on Enva summary sheet

RECEIVED
JUL-8 2000
TC 1000 MAIL ROOM

RAW SEQUENCE LISTING

DATE: 07/24/2000

PATENT APPLICATION: US/09/509,449

TIME: 13:38:40

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07242000\I509449.raw

E--> 157 ~~<230>~~ *delete*
 W--> 159 <223> OTHER INFORMATION: *← insert explanation of source material*
 159 <400> SEQUENCE: 9
 160 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile
 161 1 5 10 15
 163 <210> SEQ ID NO: 10
 164 <211> LENGTH: 1197
 165 <212> TYPE: DNA
 166 <213> ORGANISM: Artificial Sequence
 168 <220> FEATURE: *replace with <223>*
 E--> 170 ~~<230>~~ Nucleotide sequence coding for chimeric antigen
 W--> ~~172 <223> OTHER INFORMATION:~~
 172 <400> SEQUENCE: 10
 173 gaa ttc acc aaa gtg ccg gtt gct tat gcg gcc aaa ggt tat aag gtc 48
 174 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val
 175 5 10 15
 176 ctg gtt ctg gac ccg agc gtt gcc agc acc ctg ggt ttc ggc gcg tat 96
 177 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr
 178 20 25 30
 179 ctg agc aag gcc cat ggt gtg aac ccg aac atc cgc acg ggc atc cgt 144
 180 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg
 181 35 40 45
 182 acc gtt acc acc ggt gct ccg gtg acc tat tcc acc tac ggt aaa tac 192
 183 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr
 184 50 55 60
 185 ctg gcg gac ggc ggt tgc gcc ggc ggt gcg tac gat gtg atc gga tct 240
 186 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser
 187 65 70 75 80
 188 gga gag gag gtg gcc ctg tct aac act gga gag gtc ccc ttc tat ggc 288
 189 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly
 190 85 90 95
 191 cgc gcg atc ccg atc gaa gcg atc aaa ggc ggt cgc cat ctg gtt ttc 336
 192 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe
 193 100 105 110
 194 tgc cat agc aag gag aaa tgc gat gaa ctg gcg agc gcg ctg tcc gga 384
 195 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly
 196 115 120 125
 197 ttg ggt ctg aac gct gtg gca ttc tat cgc ggt ctg gac gtg agc att 432
 198 Leu Gly Leu Asn Ala Val Ala Phe Tyr Arg Gly Leu Asp Val Ser Ile
 199 130 135 140
 200 atc ccg acc cag ggc gat gtg gtt atc gtt agc acc gat gcg ctg atg 480
 201 Ile Pro Thr Gln Gly Asp Val Val Ile Val Ser Thr Asp Ala Leu Met
 202 145 150 155 160
 203 acc ggt ttt acc ggc gat ttt gac tca gtg gtc gac tgt aac aca tgc 528
 204 Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Val Asp Cys Asn Thr Cys
 205 165 170 175
 206 atc acc cag gga tct gga ctg gta agc ttc gcg agc cat gtg ccg tac 576
 207 Ile Thr Gln Gly Ser Gly Leu Val Ser Phe Ala Ser His Val Pro Tyr
 208 180 185 190

ignore

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/509,449

DATE: 07/24/2000

TIME: 13:38:40

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07242000\I509449.raw

```

209 atc gag cag ggt atg caa ctg agc gaa caa ttt aag cag aag agc ctg      624
210 ile Glu Gln Gly Met Gln Leu Ser*Glu Gln Phe Lys Gln Lys Ser Leu
211      195      200      205
212 ggt ctg ctg cag acc gcg acc aaa cag gcg gag gcg gcc gcc ccg gtg      672
213 Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Ala Pro Val
214      210      215      220
215 gtt ggc acc ccg aaa agc cgc cgt ccg gaa ggt cgt gcc tgg gcg caa      720
216 Val Gly Thr Pro Lys Ser Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln
217 225      230      235      240
218 ccg ggt acc atc atc ctg agc ggt cgt ccg gcg gtt gta ccg gat cgt      768
219 Pro Gly Thr Ile Ile Leu Ser Gly Arg Pro Ala Val Val Pro Asp Arg
220      245      250      255
221 gaa gtg ctg tat caa gaa ttt ctc gag gcc tct aga gcg gct ctc att      816
222 Glu Val Leu Tyr Gln Glu Phe Leu Glu Ala Ser Arg Ala Ala Leu Ile
223      260      265      270
224 gaa gag ggg caa ccg ata gcc gag atg ctg aag tcc aag atc cag ggc      864
225 Glu Glu Gly Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly
226      275      280      285
227 tta ctg cag caa gcc tcc aag cag gcc caa gac ata aaa atc gac ggt      912
228 Leu Leu Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Lys Ile Asp Gly
229      290      295      300
230 acc ctg att att ccg aaa gat cgt cgc agc acc ggt aaa agc tgg ggt      960
231 Thr Leu Ile Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly
232 305      310      315      320
233 aaa ccg ggc ttc ctc atc gat agc ttg cat atc aac cag cga gcc gtc      1008
234 Lys Pro Gly Phe Leu Ile Asp Ser Leu His Ile Asn Gln Arg Ala Val
235      325      330      335
236 gtt gca ccg gac aag gag gtc ctt tat gag gct ttt gat gag atg gag      1056
237 Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met Glu
238      340      345      350
239 ctc gcc atg ggc acc aac ccg aaa ccg gag cgt aaa agc aag cgt aac      1104
240 Leu Ala Met Gly Thr Asn Pro Lys Pro Glu Arg Lys Ser Lys Arg Asn
241      355      360      365
242 acc aac cgt aaa ccg cag gat att aaa ttc ccg ggt agt ggt cag gtg      1152
243 Thr Asn Arg Lys Pro Gln Asp Ile Lys Phe Pro Gly Ser Gly Gln Val
244      370      375      380
245 gtg ggt ggt gtg tac ctg gtg ccg cgt cgt ggt ccg taaggatcc      1197
246 Val Gly Gly Val Tyr Leu Val Pro Arg Arg Gly Pro
247 385      390      395
249 <210> SEQ ID NO: 11
250 <211> LENGTH: 396
251 <212> TYPE: PRT
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
E--> 256 (230) Amino acid sequence of chimeric antigen
W--> 258 <225> OTHER INFORMATION:
258 <400> SEQUENCE: 11
259 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val
260      5      10      15

```

*last sequence in file**same error**(see next page)*

RAW SEQUENCE LISTING

DATE: 07/24/2000

PATENT APPLICATION: US/09/509,449

TIME: 13:38:40

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07242000\I509449.raw

```

261 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr
262          20          25          30
263 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg
264          35          40          45
265 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr
266          50          55          60
267 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser
268 65          70          75          80
269 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly
270          85          90          95
271 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe
272          100         105         110
273 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly
274          115         120         125
275 Leu Gly Leu Asn Ala Val Ala Phe Tyr Arg Gly Leu Asp Val Ser Ile
276          130         135         140
277 Ile Pro Thr Gln Gly Asp Val Val Ile Val Ser Thr Asp Ala Leu Met
278 145          150         155         160
279 Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Val Asp Cys Asn Thr Cys
280          165         170         175
281 Ile Thr Gln Gly Ser Gly Leu Val Ser Phe Ala Ser His Val Pro Tyr
282          180         185         190
283 Ile Glu Gln Gly Met Gln Leu Ser Glu Gln Phe Lys Gln Lys Ser Leu
284          195         200         205
285 Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Pro Val
286          210         215         220
287 Val Gly Thr Pro Lys Ser Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln
288 225          230         235         240
289 Pro Gly Thr Ile Ile Leu Ser Gly Arg Pro Ala Val Val Pro Asp Arg
290          245         250         255
291 Glu Val Leu Tyr Gln Glu Phe Leu Glu Ala Ser Arg Ala Ala Leu Ile
292          260         265         270
293 Glu Glu Gly Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly
294          275         280         285
295 Leu Leu Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Lys Ile Asp Gly
296          290         295         300
297 Thr Leu Ile Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly
298 305          310         315         320
299 Lys Pro Gly Phe Leu Ile Asp Ser Leu His Ile Asn Gln Arg Ala Val
300          325         330         335
301 Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met Glu
302          340         345         350
303 Leu Ala Met Gly Thr Asn Pro Lys Pro Glu Arg Lys Ser Lys Arg Asn
304          355         360         365
305 Thr Asn Arg Lys Pro Gln Asp Ile Lys Phe Pro Gly Ser Gly Gln Val
306          370         375         380
307 Val Gly Gly Val Tyr Leu Val Pro Arg Arg Gly Pro
308 385          390         395
309 179

```

delite

See next page

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/509,449

DATE: 07/24/2000

TIME: 13:38:41

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07242000\I509449.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
 L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:118 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
 L:120 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:121 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:131 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:133 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
 L:135 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:143 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:145 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
 L:147 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:157 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
 L:159 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:170 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
 L:172 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:256 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
 L:258 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (9) Counted (11)